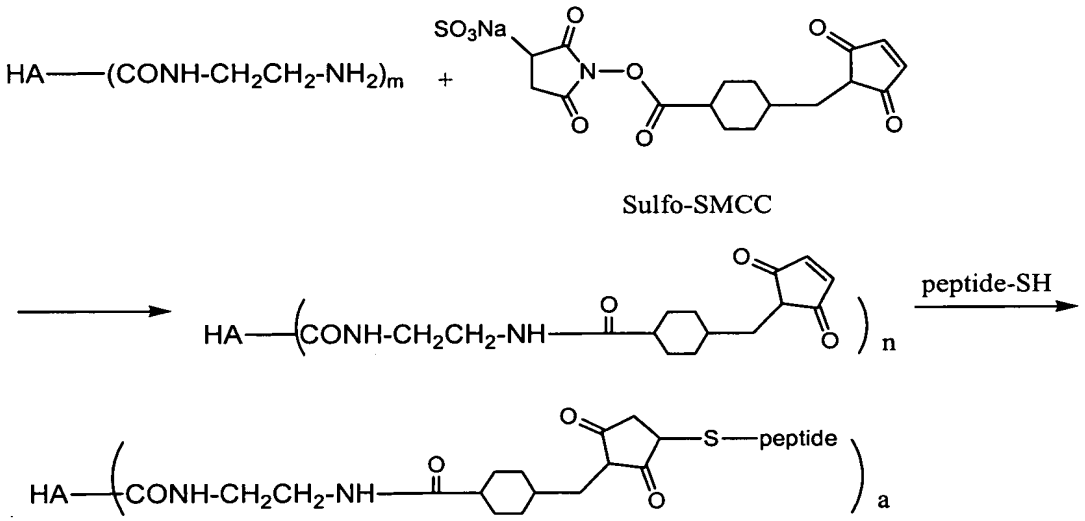
## IN THE SPECIFICATION

Please amend the third paragraph at page 43, line 10 as follows:

Publications and large public databases are available for selecting a desired epitope. In addition, conserved motifs for Class I and II epitopes are known, permitting the identification of novel epitopes within known protein sequences. Algorithms are available to the public for screening peptide sequences and peptide databases to identify Class I and II epitopes in any known sequence. (Rammensee, Bachmann, Stevanovic, MHC Ligands and Peptide Motifs, Landes Bioscience, Georgetown, TX (1997); Rammensee, Friede, Stevanovic: MHC ligands and peptide motifs: 1st listing, *Immunogenetics 41*, 178-228 (1995); Rammensee, "Cellular peptide composition governed by major histocompatibility complex class I molecules", *Nature 348*:248-251 (1990); H.G. Rammensee, J. Bachmann, N.N. Emmerich, O.A. Bachor, S. Stevanovic: SYFPEITHI: database for MHC ligands and peptide motifs. *Immunogenetics 50*: 213-219 (1999); ~~access via : http://www.uni-tuebingen.de/uni/kxi/); Thakallapally et al., "Motifscan": A Web-based Tool to Find HLA Anchor Residues in Proteins or Peptides (http://hiv-web.lan1.gov/immunology/);~~ Schreuder et al., The HLA dictionary 1999: Tissue Antigens 54:409-37(1999); ~~Hiderhiro, A compilation of anchor residue motifs available at the Graduate School of Genetic Resources Technology, Kyushu University (http://www.grt.kyushu-u.ac.jp/~hidehiro/public_old/motifs.html)~~. In addition, a prediction algorithm for proteosomal cleavages can be used to identify cleavage sites that predict intracellular epitope formation via the proteosomal pathway for presentation of class I MHC ligand ~~(*see, e.g.*, NetChop at http://www.cbs.dtu.dk/services/NetChop/, or ProPrac at http://paproc.de/)~~.

Please amend the last paragraph starting at page 55, line 20 continuing on to page 56, line 9 as follows:

Preparation of covalently linked ~~HA-protein/peptide/oligonucleotide~~ HA-peptide via thio-linkage. This approach uses the following scheme:




For this approach, dissolve 10 mg of aminonated HA in 2 ml of 0.1 M sodium phosphate, 0.15 M NaCl, pH 7.2. Add 10 molar excess of sulfo-SMCC in the above solution. Mix gently to dissolve. The mixture is put on rocker and rotated gently for 2 hours at room temperature. Immediately purify the resulting maleimide-activated HA by applying the reaction mixture to a desalting column of ~~Sephadex~~ SEPHADEX® G-25. Mix the maleimide-activated HA at the desired molar ratio with ~~peptide/protein/oligonucleotide~~ peptide dissolved in 0.1 M sodium phosphate, 0.15 M NaCl, pH 7.2, and incubate overnight. The resulting mixture is purified by dialysis or gel filtration. Final product is obtained by lyophilization.